

Detailed description of the sequence logo:
 - **X-axis:** Labeled from 610 to 800, 810 to 1000, 1010 to 1190, and 1200 to 1210.
 - **Y-axis:** Labeled A, T, C, G.
 - **Color Scale:** Red indicates high conservation, while blue indicates low conservation.
 - **Key Features:**
 - Positions 610-700: High conservation of Ile (I) and Leu (L).
 - Positions 710-800: High conservation of Val (V), Ile (I), and Leu (L).
 - Positions 810-900: High conservation of Ser (S) and Thr (T).
 - Positions 910-1000: High conservation of Asp (D) and Glu (E).
 - Positions 1010-1100: High conservation of Asp (D) and Glu (E).
 - Positions 1110-1200: High conservation of Asp (D) and Glu (E).
 - **Variants:** The logo includes sequences for 24647821.f, 24647819.f, 24647817.f, 24646073.f, 31207649.i, 6753858.m, FGFR2.h, 34859412.m, 1gjo_FGFR2, 30231254.d, 13162333.m, 6753856.m, FGFR1.h, lagw_FGFR1, 23308617.d, 17865331.m, 6679787.m, FGFR3.h, 27805803.m, 18858677.d, 34873797.m, 6679789.m, FGFR4.h, 18858679.d, 1vr2_A, 25153127.w, and 24647821.f.

	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	14
24647821.f	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
24647819.f	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
24647817.f	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
24664073.f	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
31207649.i	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
6753858.m	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
FGFR2.h	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
34859412	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
1gj_GFGR2	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
30231254.d	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
13162333.m	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
6753856.m	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
FGFR1.h	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
lagw_FGFR1	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
23308617.d	N	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	B	V
17865351.i	K	E	L	S	R	A	L	G	R	G	C	C	F	C	Q	V	M	A	R	E
6679787.m	K	E	L	S	R	A	L	G	R	G	C	C	F	C	Q	V	M	A	R	E
FGFR3.h	K	E	L	S	R	A	L	G	R	G	C	C	F	C	Q	V	M	A	R	E
27805803.k	K	E	L	S	R	A	L	G	R	G	C	C	F	C	Q	V	M	A	R	E
18858677.d	K	E	L	S	R	A	L	G	R	G	C	C	F	C	Q	V	M	A	R	E
34873797.m	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
6679789.m	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
FGFR4.h	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
18858679.d	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
1vr2_A	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
25153127.w	I	W	E	P	R	S	L	V	I	C	A	G	B	R	V	V	M	A	R	E
	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	16
24647821.f	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
24647819.f	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
24647817.f	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
24664073.f	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
31207649.i	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
6753858.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
FGFR2.h	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
34859412	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
1gj_GFGR2	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
30231254.d	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
13162333.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
6753856.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
FGFR1.h	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
lagw_FGFR1	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
23308617.d	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
17865351.i	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
6679787.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
FGFR3.h	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
27805803.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
18858677.d	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
34873797.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
6679789.m	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
FGFR4.h	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
18858679.d	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
1vr2_A	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P
25153127.w	L	A	R	D	Q	S	T	D	Y	Y	R	K	T	N	G	R	L	I	K	P

1610 1620

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24467821.f
24647819.f
24647817.f
24664073.f
31207649.i
6753858.m GS~VKT
FGFR2.h GS~VKT
34859412.m GS~VKT
1gjo_FGFR2
30231254.d GG~IKT
NG~GLNRR
13162333.m NS~GLKRR
6753856.m NG~GLKRR
FGFR1.h NG~GLKRR
lagw_FGFR1
23308617.d RGVAFKKR
17865331.m GG~PRT
GG~PRT
6679787.m GG~SRT
GG~SRT
FGFR3.h
27805803.m GG~SRT
18858677.d GV~IRT
34873797.m T
6679789.m T
FGFR4.h T
18858679.d RMDLKTTMR
1vr2_A
25153127.w NHIIITPETSQRIPSNNNMSKEEF